

EM Connectomics Cheat Sheet

website: microns-explorer.org
Info Service URL: global.daf-apis.com/info

to get list of table_names: client.materialize.get_tables()	table_name	N	short description
	synapses_pni_2	337 M	automated synapse detections
	nucleus_detection_v0	144 K	nucleus detections
	nucleus_neuron_svm	172 K	predictions about what nuclei are neurons
	aibs_soma_nuc_metamodel_preds_v117	87 K	cell type predictions about nuclei/somas
	allen_v1_column_types_slanted	1,364	manual/expert cell type calls for neurons in “column”
	aibs_column_nonneuronal	545	manual/expert cell type calls for non-neurons in “column”
	proofreading_status_public_release	764	status of axon and dendrite proofreading on cells
	functional_coreg	9,518	primary functionally coregistered cells
	func_unit_em_match_release	200	extra functionally coregistered cells

see client.materialize.get_metadata(table_name)['description'] for more

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aibs_soma_nuc_metamodel_preds_v117

Column	Description
id	The ID that is specific to cell type call annotation
target_id	the target nucleus id that this annotation references
classification_system	one aibs_neuronal, or aibs_nonneuronal indicating its broad class
cell_type	a cell type call.. see cell type table below for legend
id_ref	the nucleus id that this annotation references (should match target_id)
valid_ref	bookkeeping..can ignore
pt_supervoxel_id	a bookkeeping column for the nucleus point
pt_root_id	the ID of the segmentation at the nucleus centroid 'pt_position'
pt_position	a point that is at the centroid of the nucleus segmentation (in 4,4,40 voxels by default)

nglui.statebuilder.helpers	view_kws valid keys
make_neuron_neuroglancer_link(client, root_id(s), view_kws={}, return_as='html' or 'url') make_synapse_neuroglancer_link(synapse_df, client, view_kws={}, return_as='html' or 'url')	<ul style="list-style-type: none"><i>show_slices</i> : Boolean, sets if slices are shown in the 3d view. Defaults to False.<i>layout</i> : <i>xy-3d</i> / <i>xz-3d</i> / <i>yz-3d</i> (sections plus 3d pane), <i>xy</i> / <i>yz</i> / <i>xz</i> / <i>3d</i> (only one pane), or <i>4pane1</i> (all panes). Default is <i>xy-3d</i> .<i>show_axis_lines</i> : Boolean, determines if the axis lines are shown in the middle of each view.<i>show_scale_bar</i> : Boolean, toggles showing the scale bar.<i>orthographic</i> : Boolean, toggles orthographic view (objects are the same size no matter distance from camera) in the 3d pane.<i>position</i> : 3-element vector, determines the centered location.<i>zoom_image</i> : Zoom level for the imagery in units of nm per voxel. Defaults to 8.<i>zoom_3d</i> : Zoom level for the 3d pane. Defaults to 2000. Smaller numbers are more zoomed in.
documentation links	
caveclient docs: caveclient.readthedocs.io meshparty docs: meshparty.readthedocs.io nglui repo: https://github.com/seung-lab/NeuroglancerAnnotationUI neuroglancer: https://www.microns-explorer.org/visualization mm^3 dataset: https://www.microns-explorer.org/cortical-mm3	